Amendments to the Specification

Please amend the title of the invention on page 1 and page 75 as follows:

SCLEROTINIA-INDUCIBLE LIPID-TRANSFER POLYNUCLEOTIDES ~~GENES AND PROMOTERS~~ AND THEIR USES IN PLANT DISEASE RESISTANCE

Please amend the abstract of the invention on page 75 as follows:

Compositions and methods to aid in protecting plants from invading pathogenic organisms are provided. The compositions of the invention comprise anti-pathogenic genes, including a lipid-transfer protein encoding polynucleotide isolated from sunflower, also including their promoters, and proteins encoded by the anti-pathogenic genes. Compositions also include constructs and vectors comprising the nucleic acids, and cells, plants and seeds comprising the constructs. The compositions find use in methods for reducing or eliminating damage to plants caused by plant pathogens. Transformed plants, plant cells, tissues, and seed are also provided having newly created or enhanced disease resistance.

Please amend the paragraphs beginning on page 4, lines 22 and 24 as follows:

Figure 4 depicts the sequence of the chitinase promoter (SEQ ID NO: 5). Identified conserved regions, further discussed in the text, are indicated.

Figure 5 depicts the sequence of the LTP promoter (SEQ ID NO: 6). Identified conserved regions, further discussed in the text, are indicated.

Please amend the paragraph beginning on page 12, line 24, as follows:

Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Such implementations include but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, California); the ALIGN program (Version 2.0) and GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Version 8 (available from Genetics

Computer Group (GCG), 575 Science Drive, Madison, Wisconsin, USA). Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins *et al.* (1988) *Gene 73*:237-244 (1988); Higgins *et al.* (1989) *CABIOS 5*:151-153; Corpet *et al.* (1988) *Nucleic Acids Res. 16*:10881-90; Huang *et al.* (1992) *CABIOS 8*:155-65; and Pearson *et al.* (1994) *Meth. Mol. Biol. 24*:307-331. The ALIGN program is based on the algorithm of Myers and Miller (1988) *supra*. A PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used with the ALIGN program when comparing amino acid sequences. The BLAST programs of Altschul *et al* (1990) *J. Mol. Biol. 215*:403 are based on the algorithm of Karlin and Altschul (1990) *supra*. BLAST nucleotide searches can be performed with the BLASTN program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to a nucleotide sequence encoding a protein of the invention. BLAST protein searches can be performed with the BLASTX program, score = 50, wordlength = 3, to obtain amino acid sequences homologous to a protein or polypeptide of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res. 25*:3389. Alternatively, PSI-BLAST (in BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. See Altschul *et al.* (1997) *supra*. When utilizing BLAST, Gapped BLAST, PSI-BLAST, the default parameters of the respective programs (*e.g.*, BLASTN for nucleotide sequences, BLASTX for proteins) can be used. See ~~http://~~www.ncbi.nlm.nih.gov. Alignment may also be performed manually by inspection.

Please amend the two paragraphs beginning on page 57, line 19, as follows:

The full-length chitinase cDNA isolated from the sunflower cDNA library of *Sclerotinia*-infected sunflower leaf is 1271 bp long with an open reading frame encoding a protein of 371 amino acid residues having a molecular weight of approximately 40.8 kDa and a pI of about 8.60. A GenBank database search revealed that sunflower chitinase shares homology at the amino acid level with other plant chitinases, showing about 52% similarity and about 43% identity with a chitinase from *Nicotiana tabacum* (~~GenBank~~ SwissProt Accession No. Q43591);

about 50% similarity and 43% identity with a chitinase from *N. tabacum* (~~GenBank~~ SwissProt Accession No. Q43576); about 48% similarity and 42% identity with *Arabidopsis thaliana* chitinase (~~GenBank~~ SwissProt Accession No. Q81862).

The full-length LTP cDNA isolated from the sunflower cDNA library of *Sclerotinia*-infected sunflower leaf is 475 bp long with an open reading frame encoding a protein of 97 amino acid residues having a molecular weight of about 10.2 kDa and a pI of 8.32. A GenBank database search revealed that sunflower LTP shares homology at the amino acid level with other plant LTPs, showing about 60% similarity and about 47% identity with an LTP from *Zinnia elegans* (~~GenBank~~ SwissProt Accession No. Q42392); about 54% similarity and about 43% identity with an LTP from *Senecio odorus* (~~GenBank~~ SwissProt Accession No. Q41378); about 51% similarity and about 42% identity with *Vigna unguiculata* LTP (~~GenBank~~ SwissProt Accession No. ~~NTLP_VIGUN~~Q43681); about 49% similarity and about 40% identity with *Arabidopsis thaliana* LTP (~~GenBank~~ SwissProt Accession No. Q42158); about 53% similarity and about 40% identity with an LTP from *Brassica rapa* (~~GenBank~~ SwissProt Accession No. ~~Q~~Q64431); about 36% similarity and about 28% identity with *Hordeum vulgare* LTP (~~GenBank~~ SwissProt Accession No. ~~Q~~Q81135); about 39% similarity and about 31% identity with an LTP from *Oryza sativa* (~~GenBank~~ SwissProt Accession No. Q40631).